WHAT IS CLAIMED IS:

1 A method for detecting a chromosomal abnormality, said method comprising: quantitating the relative amount of the alleles at a heterozygous locus of interest, wherein said heterozygous locus of interest was identified by determining the sequence of alleles at a locus of interest from template DNA, wherein said relative amount is expressed as a ratio, and wherein said ratio indicates the presence or absence of a chromosomal abnormality.

2. The method of claim 1, wherein said template DNA is obtained from a source selected from the group consisting of human, non-human, mammal, reptile, cattle, cat, dog, goat, swine, pig, monkey, ape, gorilla, bull, cow, bear, horse, sheep, poultry, mouse, rat, fish, dolphin, whale, and shark.

3. The method of claim 2, wherein the template DNA is obtained from a human source.

4. The method of claim 1, wherein the template DNA is obtained from a sample selected from the group consisting of: a cell, fetal cell, tissue, blood, serum, plasma, saliva, urine, tear, vaginal secretion, umbilical cord blood, chorionic villi, amniotic fluid, embryonic tissue, an embryo, a four-celled embryo, an eight celled embryo, a 16-celled embryo, a 32-celled embryo, a 64-celled embryo, a 128-celled embryo, a 256-celled embryo, a 512-celled embryo, a 1024-celled embryo, lymph fluid, cerebrospinal fluid, mucosa secretion, peritoneal fluid, ascitic fluid, fecal matter, and body exudates.

5. The method of claim 1, wherein alleles of multiple loci of interest are sequenced and their relative amounts quantitated and expressed as a ratio.

6. The method of claim 5, wherein said multiple loci of interest are on multiple chromosomes.

7. The method of claim 3, wherein said human is a pregnant female.

8. The method of claim 7, wherein template DNA from said pregnant female is obtained from a sample selected from the group consisting of: cells, tissues, blood, serum, plasma, saliva, urine, tear, vaginal secretion, lymph fluid, cerebrospinal fluid, mucosa secretion, peritoneal fluid, ascitic fluid, fecal matter, umbilical cord blood, chorionic villi, amniotic fluid and body exudate.

9. The method of claim 4, wherein said sample is mixed with an agent that inhibits cell lysis to inhibit the lysis of cells, if cells are present, wherein the agent is selected from the group consisting of membrane stabilizer, cross-linker, and cell lysis inhibitor.

10. The method of claim 9 wherein said agent is a cell lysis inhibitor

11. The method of claim 10, wherein said cell lysis inhibitor is selected from the group consisting of glutaraldehyde, derivatives of glutaraldehyde, formaldehyde, formalin, and derivatives of formaldehyde.

12. The method of claim 9, wherein said sample is blood.

13. The method of claim 9, wherein said sample is blood from a pregnant female.

14. The method of claim 13, wherein said blood is obtained from a human pregnant female when the fetus is at a gestational age selected from the group consisting of: 0-4, 4-8, 8-12, 12-16, 16-20, 20-24, 24-28, 28-32, 32-36, 36-40, 40-44, 44-48, 48-52, and more than 52 weeks.

15. The method of claim 13, wherein said template DNA is obtained from plasma from said blood.

16. The method of claim 13, wherein said template DNA is obtained from serum from said blood.

17. The method of claim 15 or claim 16, wherein said template DNA comprises a mixture of maternal DNA and fetal DNA.

18. The method of claim 17, wherein prior to determining the sequence of alleles of a locus of interest from template DNA, maternal DNA is sequenced to identify a homozygous locus of interest, and further wherein said homozygous locus of interest is the locus of interest analyzed in the template DNA.

19. The method of claim 17, wherein prior to determining the sequence of alleles of a locus of interest from template DNA, maternal DNA is sequenced to identify a heterozygous locus of interest, and further wherein said heterozygous locus of interest is the locus of interest analyzed in the template DNA.

20. The method of claim 1, wherein determining the sequence of the alleles comprises:

(a) amplifying alleles of a locus of interest on a template DNA using a first and a second primer, wherein the second primer contains a recognition site for a restriction enzyme such that digestion with the restriction enzyme generates a 5' overhang containing the locus of interest;

(b) digesting the amplified DNA with the restriction enzyme that recognizes the recognition site on the second primer;

(c) incorporating a nucleotide into the digested DNA of (b) by using the 5' overhang containing the locus of interest as a template; and

(d) determining the sequence of the alleles of the locus of interest by determining the sequence of the DNA of (c).

21. The method of claim 1, wherein determining the sequence of alleles comprises:

(a) amplifying alleles of a locus of interest on a template DNA using a first and second primers, wherein the second primer contains a recognition site for a restriction enzyme such that digestion with the restriction enzyme generates a 5' overhang containing the locus of interest;

(b) digesting the amplified DNA with the restriction enzyme that recognizes the recognition site on the second primer;

(c) incorporating nucleotides into the digested DNA of (b), wherein;

(i) a nucleotide that terminates elongation, and is complementary to the locus of interest of an allele, is incorporated into the 5' overhang of said allele, and

(ii) a nucleotide complementary to the locus of interest of a different allele is incorporated into the 5' overhang of said different allele, and said terminating nucleotide, which is complementary to a nucleotide in the 5' overhang of said different allele, is incorporated into the 5' overhang of said different allele.

(d) determining the sequence of the alleles of a locus of interest by determining the sequence of the DNA of (c).

22. The method of claim 20 or 21, wherein the incorporation of a nucleotide in (c) is by a DNA polymerase selected from the group consisting of E. coli DNA polymerase, Klenow fragment of E. coli DNA polymerase I, T7 DNA polymerase, T4 DNA polymerase, Taq polymerase, Pfu DNA polymerase, Vent DNA polymerase and sequenase.

23. The method of claim 20, wherein the incorporation of a nucleotide in (c) comprises incorporation of a labeled nucleotide.

24. The method of claim 20, wherein the incorporation of a nucleotide in (c) comprises incorporation of a dideoxynucleotide.

25. The method of claim 20, wherein the incorporation of a nucleotide in (c) further comprises incorporation of a deoxynucleotide and a dideoxynucleotide.

26. The method of claim 1, wherein the incorporation of a nucleotide in (c) further comprises using a mixture of labeled and unlabeled nucleotides.

27. The method of claim 23, wherein the labeled nucleotide is labeled with a molecule selected from the group consisting of radioactive molecule, fluorescent molecule, antibody, antibody fragment, hapten, carbohydrate, biotin, derivative of biotin, phosphorescent moiety, luminescent moiety, electrochemiluminescent moiety, chromatic moiety, and moiety having a detectable electron spin resonance, electrical capacitance, dielectric constant and electrical conductivity.

28. The method of claim 27, wherein the labeled nucleotide is labeled with a fluorescent molecule.

29. The method of claim 21, wherein the incorporation of a nucleotide in (c)(i) comprises incorporation of a labeled nucleotide.

30. The method of claim 21, wherein the incorporation of a nucleotide in (c)(i) comprises incorporation of a dideoxynucleotide.

31. The method of claim 21, wherein the incorporation of a nucleotide in (c)(i) further comprises incorporation of a deoxynucleotide and a dideoxynucleotide.

32. The method of claim 21, wherein the incorporation of a nucleotide in (c)(i) further comprises using a mixture of labeled and unlabeled nucleotides.

33. The method of claim 21, wherein the incorporation of a nucleotide in (c)(ii) comprises incorporation of a labeled nucleotide.

34. The method of claim 21, wherein the incorporation of a nucleotide in (c)(ii) comprises incorporation of a deoxynucleotide.

35. The method of claim 21, wherein the incorporation of a nucleotide in (c)(ii) further comprises incorporation of a deoxynucleotide and a dideoxynucleotide.

36. The method of claim 21, wherein the incorporation of a nucleotide in (c)(ii) further comprises using a mixture of labeled and unlabeled nucleotides.

37. The method of claim 29, wherein the labeled nucleotide is a dideoxynucleotide.

38. The method of claim 29, wherein the labeled nucleotide is labeled with a molecule selected from the group consisting of radioactive molecule, fluorescent molecule, antibody, antibody fragment, hapten, carbohydrate, biotin, derivative of biotin, phosphorescent moiety, luminescent moiety, electrochemiluminescent moiety, chromatic moiety, and moiety having a detectable electron spin resonance, electrical capacitance, dielectric constant and electrical conductivity.

39. The method of claim 38, wherein the labeled nucleotide is labeled with a fluorescent molecule.

40. The method of claim 39, wherein the incorporation of a nucleotide in (c)(i) further comprises incorporation of an unlabeled nucleotide.

41. The method of claim 20 or 21, wherein the determination of the sequence of the locus of interest in (d) comprises detecting a nucleotide.

42. The method of claim 20 or 21, wherein said first and second primers contain a portion of a restriction enzyme recognition site that contains a variable nucleotide, wherein the full restriction enzyme recognition site is generated after amplification.

43. The method of claim 20 or 21, wherein the restriction enzyme recognition site is for a restriction enzyme selected from the group consisting of BsaJ I, Bssk I, Dde I, EcoN I, Fnu4H I, Hinf I, and ScrF I.

44. The method of claim 20 or 21, wherein the restriction enzyme cuts DNA at a distance from the recognition site.

45. The method of claim 44, wherein the recognition site is for a Type IIS restriction enzyme.

46. The method of claim 45, wherein the Type IIS restriction enzyme is selected from the group consisting of: Alw I, Alw26 I, Bbs I, Bbv I, BceA I, Bmr I, Bsa I, Bst71 I, BsmA I, BsmB I, BsmF I, BspM I, Ear I, Fau I, Fok I, Hga I, Ple I, Sap I, SSfaN I, and Sthi32 I.

47. The method of claim 20 or 21, wherein said method of amplification is selected from the group consisting of: polymerase chain reaction, self-sustained sequence reaction, ligase chain reaction, rapid amplification of cDNA ends, polymerase chain reaction and ligase chain reaction, Q-beta phage amplification, strand displacement amplification, and splice overlap extension polymerase chain reaction.

48. The method of claim 47, wherein said method of amplification is PCR.

49. The method of claim 48, wherein an annealing temperature for cycle 1 of PCR is about the melting temperature of the portion of the 3' region of the second primer that anneals to the template DNA.

50. The method of claim 49, wherein an annealing temperature for cycle 2 of PCR is about the melting temperature of the portion of the 3' region of the first primer that anneals to the template DNA.

51. The method of claim 50, wherein an annealing temperature for the remaining cycles of PCR is at about the melting temperature of the entire second primer.

52. The method of claim 1, wherein determining the sequence comprises a method selected from the group consisting of: allele specific PCR, mass spectrometry, hybridization, primer extension, fluorescence resonance energy transfer (FRET), sequencing, Sanger dideoxy sequencing, DNA microarray, GeneCHIP arrays, HuSNP arrays, CodeLink Arrays, BeadArray Technology, MassARRAY, MassEXTEND, SNP-IT, TaqMan, InvaderStrand Assay, southern blot, slot blot, dot blot, and MALDI-TOF mass spectrometry.

53. The method of claim 1, wherein said ratio for alleles at heterozygous loci of interest on a chromosome are summed and compared to the ratio for alleles at heterozygous loci of interest on a different chromosome, wherein a difference in ratios indicates the presence of a chromosomal abnormality.

54. The method of claim 53, wherein the chromosomes that are compared are human chromosomes selected from the group consisting of: chromosome 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, X, and Y.

55. The method of claim 53, wherein the ratio for the alleles at heterozygous loci of interest of chromosomes 13, 18, and 21 are compared.

56. The method of claim 1, wherein said locus of interest is a single nucleotide polymorphism.

57. The method of claim 1, wherein said locus of interest is a mutation.

58. A method comprising determining the sequence of a locus of interest on free fetal DNA from a sample comprising free fetal DNA, wherein agent that inhibits cell lysis has been added to said

sample to inhibit lysis of cells, if cells are present, wherein said agent is selected from the group consisting of membrane stabilizer, cross-linker, and cell lysis inhibitor.

59. The method of claim 58, wherein said sample is selected from the group consisting of: tissue, cell, blood, serum, plasma, urine, and vaginal secretion.

60. The method of claim 59, wherein said sample is blood.

61. The method of claim 58, wherein said sample comprises free maternal template DNA and free fetal template DNA.

62. The method of claim 58, wherein said agent is a cell lysis inhibitor.

63. The method of claim 62, wherein said cell lysis inhibitor is selected from the group consisting of: glutaraldehyde, derivatives of glutaraldehyde, formaldehyde, derivatives of formaldehyde, and formalin.

64. The method of claim 58, wherein prior to determining the sequence, template DNA was isolated.

65. The method of claim 60, wherein said template DNA is obtained from plasma of said blood.

66. The method of claim 60, wherein said template DNA is obtained from serum of said blood.

67. The method of claim 58, wherein prior to determining the sequence of the locus of interest on fetal DNA , the sequence of the locus of interest on maternal template DNA was determined.

68. The method of claim 58, wherein prior to determining the sequence of the locus of interest on fetal DNA, the sequence of the locus of interest on paternal template DNA was determined.

69. The method of claim 58, wherein said locus of interest is a single nucleotide polymorphism.

70. The method of claim 58, wherein said locus of interest is a mutation.

71. The method of claim 58, wherein the sequence of multiple loci of interest is determined.

72. The method of claim 71, wherein the multiple loci of interest are on multiple chromosomes.

73. The method of claim 58, wherein determining the sequence comprises:

(a) amplifying a locus of interest on a template DNA using a first and second primers, wherein the second primer contains a recognition site for a restriction enzyme such that digestion with the restriction enzyme generates a 5' overhang containing the locus of interest;

(b) digesting the amplified DNA with the restriction enzyme that recognizes the recognition site on the second primer;

(c) incorporating a nucleotide into the digested DNA of (b) by using the 5' overhang containing the locus of interest as a template; and

(d) determining the sequence of the locus of interest by determining the sequence of the DNA of (c).

74. The method of claim 58, wherein determining the sequence comprises:

(a) amplifying alleles of a locus of interest on a template DNA using a first and second primers, wherein the second primer contains a recognition site for a restriction enzyme such that digestion with the restriction enzyme generates a 5' overhang containing the locus of interest;

(b) digesting the amplified DNA with the restriction enzyme that recognizes the recognition site on the second primer;

(c) incorporating nucleotides into the digested DNA of (b), wherein;

(i) a nucleotide that terminates elongation, and is complementary to the locus of interest of an allele, is incorporated into the 5' overhang of said allele, and

(ii) a nucleotide complementary to the locus of interest of a different allele is incorporated into the 5' overhang of said different allele, and said terminating nucleotide, which is

complementary to a nucleotide in the 5' overhang of said different allele, is incorporated into the 5' overhang of said different allele.

(d) determining the sequence of the alleles of a locus of interest by determining the sequence of the DNA of (c).

75. The method of claim 73 or 74, wherein the restriction enzyme cuts DNA at a distance from the recognition site.

76. The method of claim 75, wherein the recognition site is for a Type IIS restriction enzyme.

77. The method of claim 76, wherein the Type IIS restriction enzyme is selected from the group consisting of: Alw I, Alw26 I, Bbs I, Bbv I, BceA I, Bmr I, Bsa I, Bst71 I, BsmA I, BsmB I, BsmF I, BspM I, Ear I, Fau I, Fok I, Hga I, Ple I, Sap I, SSfaN I, and Sthi32 I.

78. The method of claim 73 or 74, wherein said method of amplification is selected from the group consisting of: polymerase chain reaction, self-sustained sequence reaction, ligase chain reaction, rapid amplification of cDNA ends, polymerase chain reaction and ligase chain reaction, Q-beta phage amplification, strand displacement amplification, and splice overlap extension polymerase chain reaction.

79. The method of claim 78, wherein said method of amplification is by PCR.

80. The method of claim 79, wherein an annealing temperature for cycle 1 of PCR is about the melting temperature of the portion of the 3' region of the second primer that anneals to the template DNA.

81. The method of claim 80, wherein an annealing temperature for cycle 2 of PCR is about the melting temperature of the portion of the 3' region of the first primer that anneals to the template DNA.

82. The method of claim 81, wherein an annealing temperature for the remaining cycles of PCR is at about the melting temperature of the entire second primer.

83. The method of claim 58, wherein the sequence of a locus of interest was determined using a method selected from the group consisting of: allele specific PCR, mass spectrometry, hybridization,

primer extension, fluorescence polarization, fluorescence resonance energy transfer (FRET), fluorescence detection, sequencing, Sanger dideoxy sequencing, DNA micorarray, southern blot, slot blot, dot blot, and MALDI-TOF mass spectrometry.

84. A method for determining the sequence of a locus of interest in a sample comprising fetal DNA, said method comprising:

(a) amplifying a locus of interest on a template DNA using a first and second primers, wherein the second primer contains a recognition site for a restriction enzyme such that digestion with the restriction enzyme generates a 5' overhang containing the locus of interest;

(b) digesting the amplified DNA with the restriction enzyme that recognizes the recognition site on the second primer;

(c) incorporating a nucleotide into the digested DNA of (b) by using the 5' overhang containing the locus of interest as a template; and

(d) determining the sequence of the locus of interest by determining the sequence of the DNA of (c).

85. A method for determining the sequence of a locus of interest in a sample comprising fetal DNA, said method comprising:

(a) amplifying alleles of a locus of interest on a template DNA using a first and second primers, wherein the second primer contains a recognition site for a restriction enzyme such that digestion with the restriction enzyme generates a 5' overhang containing the locus of interest;

(b) digesting the amplified DNA with the restriction enzyme that recognizes the recognition site on the second primer;

(c) incorporating nucleotides into the digested DNA of (b), wherein;

(i) a nucleotide that terminates elongation, and is complementary to the locus of interest of an allele, is incorporated into the 5' overhang of said allele, and

(ii) a nucleotide complementary to the locus of interest of a different allele is incorporated into the 5' overhang of said different allele, and said terminating nucleotide, which is complementary to a nucleotide in the 5' overhang of said different allele, is incorporated into the 5' overhang of said different allele.

(d) determining the sequence of the alleles of a locus of interest by determining the sequence of the DNA of (c).

86. The method of claim 84 or claim 85, wherein said sample is selected from the group consisting of cell, tissue, blood, serum, plasma, saliva, urine, tears, vaginal secretion, sweat, umbilical cord blood, chorionic villi, amniotic fluid, embryonic tissue, embryo, a two-celled embryo, a four-celled embryo, an eight-celled embryo, a 16-celled embryo, a 32- celled embryo, a 64-celled embryo, a 128-celled embryo, a 256-celled embryo, a 512-celled embryo, a 1024-celled embryo, lymph fluid, cerebrospinal fluid, mucosa secretion, peritoneal fluid, ascitic fluid, fecal matter, and body exudates.

87. A method for preparing a sample for analysis comprising isolating free nucleic acid from a sample that contains nucleic acid, wherein an agent that inhibits cell lysis inhibitor has been added to the sample to inhibit lysis of cells, if cells are present, and wherein said agent is selected from the group consisting of membrane stabilizer, cross-linker, and cell lysis inhibitor.

88. The method of claim 87, wherein said sample is obtained from a source selected from the group consisting of human, non-human, mammal, reptile, cattle, cat, dog, goat, swine, pig, monkey, ape, gorilla, bull, cow, bear, horse, sheep, poultry, mouse, rat, fish, dolphin, whale, and shark.

89. The method of claim 88, wherein the sample is obtained from a human source.

90. The method of claim 87, wherein the sample is obtained from a source selected from the group consisting of: a cell, fetal cell, tissue, blood, serum, plasma, saliva, urine, tear, vaginal secretion, umbilical cord blood, chorionic villi, amniotic fluid, embryonic tissue, lymph fluid, cerebrospinal fluid, mucosa secretion, peritoneal fluid, ascitic fluid, fecal matter, and body exudates.

91. The method of claim 90, wherein said sample is blood.

92. The method of claim 91, wherein said blood is from a pregnant female.

93. The method of claim 92, wherein said blood is obtained from a human pregnant female when the fetus is at a gestational age selected from the group consisting of: 0-4, 4-8, 8-12, 12-16, 16-20, 20-24, 24-28, 28-32, 32-36, 36-40, 40-44, 44-48, 48-52, and more than 52 weeks.

94. The method of claim 93, wherein said sample is obtained from plasma from said blood.

95. The method of claim 87, wherein said agent is a cell lysis inhibitor.

96. The method of claim 87, wherein said cell lysis inhibitor is selected from the group consisting of glutaraldehyde, derivatives of glutaraldehyde, formaldehyde, formalin, and derivatives of formaldehyde.

97. The method of claim 96, wherein said cell lyis inhibitor is formalin.

98. The method of claim 97, wherein the final concentration of formalin in the sample is selected from the group consisting of: 0.0001-0.03%, 0.03-0.05%, 0.05-0.08%, 0.08-0.1%, 0.1-0.3%, 0.3-0.5%, 0.5-0.7%, 0.7-0.9%, 0.9-1.2%, 1.2-1.5%, 1.5-2%, and 2-3%.

99. The method of claim 98, wherein the final concentration of formalin in the sample is 0.1%.

100. The method of claim 87, wherein isolation of nucleic acid comprises a centrifugation step.

101. The method of claim 100, wherein the centrifugation step is performed with the centrifuge braking power set to zero.

102. The method of claim 100, wherein the centrifugation step is performed at a speed selected from the group consisting of 0-50 rpm, 50-100 rpm, 100-200 rpm, 200-300 rpm, 300-400 rpm, 400-500 rpm, 500-600 rpm, 600-700 rpm, 700-800 rpm, 800-900 rpm, 900-1000 rpm, 1000-2000 rpm, 2000-3000 rpm, 3000-4000 rpm, 4000-5000 rpm, 5000-6000 rpm, 6000-7000 rpm, 7000-8000 rpm, and greater than 8000 rpm.

103. The method of claim 1 wherein said sequence is determined by a method comprising:

(1) amplification of the locus of interest;

(2) hybridization of amplified loci to GeneCHIP array

(3) washing GeneCHIP array;

(4) staining the GeneCHIP array with detectable reagents; and

(5) scanning GeneCHIP array.

104. The method of claim 58, wherein said sequence is determined by a method comprising:

(1) amplification of the locus of interest;

(2) hybridization of amplified loci to GeneCHIP array

(3) washing GeneCHIP array;

(4) staining the GeneCHIP array with detectable reagents; and

(5) scanning GeneCHIP array.

105. The method of claim 103 or 104, wherein the amplification method in (a)(1) is selected from the group consisting of: polymerase chain reaction, self-sustained sequence reaction, ligase chain reaction, rapid amplification of cDNA ends, polymerase chain reaction and ligase chain reaction, Q-beta phage amplification, strand displacement amplification, and splice overlap extension polymerase chain reaction.

106. The method of claim 105, wherein said method of amplification is by PCR.

107. The method of claim 103 or 104, wherein said staining method comprises streptavidin phycoerhthrin and biotinylated anti-streptavidin.

108. The method of claim 1, wherein said sequence is determined by a method comprising:

(1) amplification of the locus of interest;

(2) amplicon fragmentation;

(3) hybridization of fragmented amplicons to CodeLink Arrays;

(4) extension reaction to incorporate a nucleotide; and

(5) detection of incorporated nucleotides.

109. The method of claim 58, wherein said sequence is determined by a method comprising:

(1) amplification of the locus of interest;

(2) amplicon fragmentation;

(3) hybridization of fragmented amplicons to CodeLink Arrays;

(4) extension reaction to incorporate a nucleotide; and

(5) detection of incorporated nucleotides.

110. The method of claim 108 or 109 wherein the amplification method is selected from the group consisting of: polymerase chain reaction, self-sustained sequence reaction, ligase chain reaction, rapid amplification of cDNA ends, polymerase chain reaction and ligase chain reaction, Q-beta phage amplification, strand displacement amplification, and splice overlap extension polymerase chain reaction.

111. The method of claim 110, wherein said method of amplification is by PCR.

112. The method of claim 108 or 109, wherein said amplicon fragmentation is by exonuclease digestion.

113. The method of claim 108 or 109, wherein said incorporated nucleotide is a dideoxynucleotide or deoxynucleotide.

114. The method of claim 113, wherein said incorporated nucleotide is labeled with a molecule selected from the group consisting of radioactive molecule, fluorescent molecule, antibody, antibody fragment, hapten, carbohydrate, biotin, derivative of biotin, phosphorescent moiety, luminescent moiety, electrochemiluminescent moiety, chromatic moiety, and moiety having a detectable electron spin resonance, electrical capacitance, dielectric constant and electrical conductivity.

115. The method of claim 114, wherein the labeled nucleotide is labeled with a fluorescent molecule.

116. The method of claim 1, wherein said sequence is determined by a method comprising: using BeadArray Technology.

117. The method of claim 58, wherein said sequence is determined by a method comprising: using BeadArray Technology.

118. The method of claim 1, wherein said sequence is determined by a method comprising:
(1) amplification of the locus of interest;

(2) dephosphorylation of the unused reagents in (a);

(3) in vitro transcription reaction of the products of (b);

(4) RNase A cleavage of the products of (c);

(5) mixing the products of (d) with CleanResin;

(6) transfer products of (e) to SpectroCHIP; and

(7) analysis of the SpectroCHIP.

119. The method of claim 58, wherein said sequence is determined by a method comprising:

(1) amplification of the locus of interest;

(2) dephosphorylation of the unused reagents in (a);

(3) in vitro transcription reaction of the products of (b);

(4) RNase A cleavage of the products of (c);

(5) mixing the products of (d) with CleanResin;

(6) transfer products of (e) to SpectroCHIP; and

(7) analysis of the SpectroCHIP.

120. The method of claim 118 or 119, wherein the amplification method is selected from the group consisting of: polymerase chain reaction, self-sustained sequence reaction, ligase chain reaction, rapid amplification of cDNA ends, polymerase chain reaction and ligase chain reaction, Q-beta phage amplification, strand displacement amplification, and splice overlap extension polymerase chain reaction.

121. The method of claim 120, wherein said method of amplification is by PCR.

122. The method of claim 118 or 119, wherein said dephosphorylation reaction is with shrimp alkaline phosphatase.

123. The method of claim 1, wherein said sequence is determined by a method comprising:

(1) amplification of a locus of interest;

(2) dephosphorylation of the unused reagents in (a);

(3) hybridization of a primer to the locus of interest;

(4) incorporation of a nucleotide;

(5) mixing the products of (d) with CleanResin;

(6) transfer products of (e) to SpectroCHIP; and

(7) analysis of the SpectroCHIP.

124. The method of claim 58, wherein said sequence is determined by a method comprising:

(1) amplification of a locus of interest;

(2) dephosphorylation of the unused reagents in (a);

(3) hybridization of a primer to the locus of interest;

(4) incorporation of a nucleotide;

(5) mixing the products of (d) with CleanResin;

(6) transfer products of (e) to SpectroCHIP; and

(7) analysis of the SpectroCHIP.

125. The method of claim 123 or 124, wherein the amplification method is selected from the group consisting of: polymerase chain reaction, self-sustained sequence reaction, ligase chain reaction, rapid amplification of cDNA ends, polymerase chain reaction and ligase chain reaction, Q-beta phage amplification, strand displacement amplification, and splice overlap extension polymerase chain reaction.

126. The method of claim 125, wherein said method of amplification is by PCR.

127. The method of claim 123 or 124, wherein said dephosphorylation reaction is catalyzed by shrimp alkaline phosphatase.

128. The method of claim 123 or 124, wherein said hybridization of primer is adjacent to the locus of interest.

129. The method of claim 123 or 124, wherein said incorporated nucleotide is a dideoxynucleotide or deoxynucleotide.

130. The method of claim 129, wherein said incorporated nucleotide is labeled with a molecule selected from the group consisting of radioactive molecule, fluorescent molecule, antibody, antibody fragment, hapten, carbohydrate, biotin, derivative of biotin, phosphorescent moiety, luminescent moiety,

electrochemiluminescent moiety, chromatic moiety, and moiety having a detectable electron spin resonance, electrical capacitance, dielectric constant and electrical conductivity.

131. The method of claim 130, wherein the labeled nucleotide is labeled with a fluorescent molecule.

132. The method of claim 1, wherein said sequence is determined by a method comprising:
(1) amplification of the locus of interest;
(2) exonuclease treatment of the products of (1);
(3) single stranded DNA of (2) is annealed to an oligonucleotide;
(4) incorporation of a nucleotide using the annealed template and primer of (3);
(5) detection of the incorporated nucleotide.

133. The method of claim 58, wherein said sequence is determined by a method comprising:
(1) amplification of the locus of interest;
(2) exonuclease treatment of the products of (1);
(3) single stranded DNA of (2) is annealed to an oligonucleotide;
(4) incorporation of a nucleotide using the annealed template and primer of (3);
(5) detection of the incorporated nucleotide.

134. The method of claim 132 or 133, wherein the amplification method is selected from the group consisting of: polymerase chain reaction, self-sustained sequence reaction, ligase chain reaction, rapid amplification of cDNA ends, polymerase chain reaction and ligase chain reaction, Q-beta phage amplification, strand displacement amplification, and splice overlap extension polymerase chain reaction.

135. The method of claim 134, wherein said method of amplification is by PCR.

136. The method of claim 132 or 133, wherein said primer hybridizes adjacent to the locus of interest.

137. The method of claim 132 or 133, wherein said incorporated nucleotide is a dideoxynucleotide or deoxynucleotide.

138. The method of claim 132 or 133, wherein said incorporation reaction comprises two terminating nucleotides and two non-terminating nucleotides.

139. The method of claim 137, wherein said incorporated nucleotide is labeled with a molecule selected from the group consisting of radioactive molecule, fluorescent molecule, antibody, antibody fragment, hapten, carbohydrate, biotin, derivative of biotin, phosphorescent moiety, luminescent moiety, electrochemiluminescent moiety, chromatic moiety, and moiety having a detectable electron spin resonance, electrical capacitance, dielectric constant and electrical conductivity.

140. The method of claim 138, wherein said terminating nucleotides are labeled with a molecule selected from the group consisting of radioactive molecule, fluorescent molecule, antibody, antibody fragment, hapten, carbohydrate, biotin, derivative of biotin, phosphorescent moiety, luminescent moiety, electrochemiluminescent moiety, chromatic moiety, and moiety having a detectable electron spin resonance, electrical capacitance, dielectric constant and electrical conductivity.

141. The method of claim 139, wherein the labeled nucleotide is labeled with a fluorescent molecule.

142. The method of claim 140, wherein the terminating nucleotides are labeled with a fluorescent molecule.

143. The method of claim 1, wherein said sequence is determined by a method comprising:

(1) amplification of the locus of interest, wherein the amplification reaction comprises a forward primer, a reverse primer, and a probe that anneals to the locus of interest, which is within the region of the amplicon; and

(2) detection of the PCR products, wherein the amount of PCR product is used to determine the presence or absence of a specific genetic sequence.

144. The method of claim 58, wherein said sequence is determined by a method comprising:

(1) amplification of the locus of interest, wherein the amplification reaction comprises a forward primer, a reverse primer, and a probe that anneals to the locus of interest, which is within the region of the amplicon; and

(2) detection of the PCR products, wherein the amount of PCR product is used to determine the presence or absence of a specific genetic sequence.

145. The method of claim 143 or 144, wherein the amplification is by PCR.

146. The method of claim 143 or 144, wherein the probe contains a reporter dye at the 5' end and the 3' end contains a quenching dye.

147. The method of claim 143 or 144, wherein the PCR products are detected using the ABI 7700 Sequence Detection System.

148. The method of claims 103, 104 108, 109, 116, 117, 118, 119, 123, 124, 132, 133, 143 or 144, wherein an agent that inhibits cell lysis has been added to the sample to inhibit the lysis of cells, if present, and wherein said agent is selected from the group consisting of membrane stabilizer, cross-linker, and cell lysis inhibitor.

149. The method of claim 141, wherein said agent is a cell lysis inhibitor.

150. The method of claim 141, wherein said cell lysis inhibitor is formalin at a percentage selected from the group consisting of: 0.0001-0.03%, 0.03-0.05%, 0.05-0.08%, 0.08-0.1%, 0.1-0.3%, 0.3-0.5%, 0.5-0.7%, 0.7-0.9%, 0.9-1.2%, 1.2-1.5%, 1.5-2%, and 2-3%.

151. The method of claim 142, wherein the concentration of formalin in the sample is 0.1%.

152. A method for detecting a chromosomal abnormality, said method comprising:

(a) determining the sequence of alleles of a locus of interest from template DNA,

(b) quantitating the relative amount of the alleles at a heterozygous locus of interest that was identified from the locus of interest of (a), wherein said relative amount is expressed as a ratio, and wherein said ratio indicates the presence or absence of a chromosomal abnormality.

153. A composition comprising fetal DNA and maternal DNA, wherein the percentage of free fetal DNA in the total free DNA of the composition is selected from the group consisting of: about 15-16% fetal DNA, about 16-17% fetal DNA, about 17-18% fetal DNA, about 18-19% fetal DNA, about 19-20% fetal DNA, about 20-21% fetal DNA, about 21-22% fetal DNA, about 22-23% fetal DNA, about 23-24% fetal DNA, about 24-25% fetal DNA, about 25-35% fetal DNA, about 35-45% fetal DNA, about 45-55% fetal DNA, about 55-65% fetal DNA, about 65-75% fetal DNA, about 75-85% fetal DNA, about 85-90% fetal DNA, about 90-91% fetal DNA, about 91-92% fetal DNA, about 92-93% fetal DNA, about 93-94% fetal DNA, about 94-95% fetal DNA, about 95-96% fetal DNA, about 96-97% fetal DNA, about 97-98% fetal DNA, about 98-99% fetal DNA, and about 99-99.7% fetal DNA.

154. A composition comprising fetal DNA and maternal DNA, wherein the percentage of free fetal DNA in the total free DNA of the composition is selected from the group consisting of: about 15-16% fetal DNA, about 16-17% fetal DNA, about 17-18% fetal DNA, about 18-19% fetal DNA, about 19-20% fetal DNA, about 20-21% fetal DNA, about 21-22% fetal DNA, about 22-23% fetal DNA, about 23-24% fetal DNA, about 24-25% fetal DNA, about 25-35% fetal DNA, about 35-45% fetal DNA, about 45-55% fetal DNA, about 55-65% fetal DNA, about 65-75% fetal DNA, about 75-85% fetal DNA, about 85-90% fetal DNA, about 90-91% fetal DNA, about 91-92% fetal DNA, about 92-93% fetal DNA, about 93-94% fetal DNA, and about 94-95% fetal DNA.

155. A prenatal diagnostic method comprising analyzing a composition comprising fetal DNA and maternal DNA, wherein the percentage of free fetal DNA in the total free DNA of the composition is selected from the group consisting of: about 15-16% fetal DNA, about 16-17% fetal DNA, about 17-18% fetal DNA, about 18-19% fetal DNA, about 19-20% fetal DNA, about 20-21% fetal DNA, about 21-22% fetal DNA, about 22-23% fetal DNA, about 23-24% fetal DNA, about 24-25% fetal DNA, about 25-35% fetal DNA, about 35-45% fetal DNA, about 45-55% fetal DNA, about 55-65% fetal DNA, about 65-75% fetal DNA, about 75-85% fetal DNA, about 85-90% fetal DNA, about 90-91% fetal DNA, about 91-92% fetal DNA, about 92-93% fetal DNA, about 93-94% fetal DNA, and about 94-95% fetal DNA.

156. A kit for use in the method of any of claims 1-16, 20, 21, 23-40, 52-74, 83, 84, or 85 comprising a set of primers used in the method, wherein the second primer contains a sequence that

generates a recognition site for a restriction enzyme such that digestion with the restriction enzyme generates a 5"overhang containing the locus of interest, and a set of instructions.

157. A kit for use in the method of claim 17, comprising a set of primers used in the method, wherein the second primer contains a sequence that generates a recognition site for a restriction enzyme such that digestion with the restriction enzyme generates a 5'overhang containing the locus of interest, and a set of instructions.

158. A kit for use in the method of claim 18, comprising a set of primers used in the method, wherein the second primer contains a sequence that generates a recognition site for a restriction enzyme such that digestion with the restriction enzyme generates a 5'overhang containing the locus of interest, and a set of instructions.

159. A kit for use in the method of claim 19, comprising a set of primers used in the method, wherein the second primer contains a sequence that generates a recognition site for a restriction enzyme such that digestion with the restriction enzyme generates a 5'overhang containing the locus of interest, and a set of instructions.

160. A kit for use in the method of claim 22, comprising a set of primers used in the method, wherein the second primer contains a sequence that generates a recognition site for a restriction enzyme such that digestion with the restriction enzyme generates a 5'overhang containing the locus of interest, and a set of instructions.

161. A kit for use in the method of claim 41, comprising a set of primers used in the method, wherein the second primer contains a sequence that generates a recognition site for a restriction enzyme such that digestion with the restriction enzyme generates a 5'overhang containing the locus of interest, and a set of instructions.

162. A kit for use in the method of claim 42, comprising a set of primers used in the method, wherein the second primer contains a sequence that generates a recognition site for a restriction enzyme such that digestion with the restriction enzyme generates a 5'overhang containing the locus of interest, and a set of instructions.

163. A kit for use in the method of claim 43, comprising a set of primers used in the method, wherein the second primer contains a sequence that generates a recognition site for a restriction enzyme such that digestion with the restriction enzyme generates a 5'overhang containing the locus of interest, and a set of instructions.

164. A kit for use in the method of claim 44, comprising a set of primers used in the method, wherein the second primer contains a sequence that generates a recognition site for a restriction enzyme such that digestion with the restriction enzyme generates a 5'overhang containing the locus of interest, and a set of instructions.

165. A kit for use in the method of claim 45, comprising a set of primers used in the method, wherein the second primer contains a sequence that generates a recognition site for a restriction enzyme such that digestion with the restriction enzyme generates a 5'overhang containing the locus of interest, and a set of instructions.

166. A kit for use in the method of claim 46, comprising a set of primers used in the method, wherein the second primer contains a sequence that generates a recognition site for a restriction enzyme such that digestion with the restriction enzyme generates a 5'overhang containing the locus of interest, and a set of instructions.

167. A kit for use in the method of claim 47, comprising a set of primers used in the method, wherein the second primer contains a sequence that generates a recognition site for a restriction enzyme such that digestion with the restriction enzyme generates a 5'overhang containing the locus of interest, and a set of instructions.

168. A kit for use in the method of claim 48, comprising a set of primers used in the method, wherein the second primer contains a sequence that generates a recognition site for a restriction enzyme such that digestion with the restriction enzyme generates a 5'overhang containing the locus of interest, and a set of instructions.

169. A kit for use in the method of claim 49, comprising a set of primers used in the method, wherein the second primer contains a sequence that generates a recognition site for a restriction enzyme such that digestion with the restriction enzyme generates a 5'overhang containing the locus of interest, and a set of instructions.

170. A kit for use in the method of claim 50, comprising a set of primers used in the method, wherein the second primer contains a sequence that generates a recognition site for a restriction enzyme such that digestion with the restriction enzyme generates a 5'overhang containing the locus of interest, and a set of instructions.

171. A kit for use in the method of claim 51, comprising a set of primers used in the method, wherein the second primer contains a sequence that generates a recognition site for a restriction enzyme such that digestion with the restriction enzyme generates a 5'overhang containing the locus of interest, and a set of instructions.

172. A kit for use in the method of claim 75, comprising a set of primers used in the method, wherein the second primer contains a sequence that generates a recognition site for a restriction enzyme such that digestion with the restriction enzyme generates a 5'overhang containing the locus of interest, and a set of instructions.

173. A kit for use in the method of claim 76, comprising a set of primers used in the method, wherein the second primer contains a sequence that generates a recognition site for a restriction enzyme such that digestion with the restriction enzyme generates a 5'overhang containing the locus of interest, and a set of instructions.

174. A kit for use in the method of claim 77, comprising a set of primers used in the method, wherein the second primer contains a sequence that generates a recognition site for a restriction enzyme such that digestion with the restriction enzyme generates a 5'overhang containing the locus of interest, and a set of instructions.

175. A kit for use in the method of claim 78, comprising a set of primers used in the method, wherein the second primer contains a sequence that generates a recognition site for a restriction enzyme

such that digestion with the restriction enzyme generates a 5'overhang containing the locus of interest, and a set of instructions.

176. A kit for use in the method of claim 79, comprising a set of primers used in the method, wherein the second primer contains a sequence that generates a recognition site for a restriction enzyme such that digestion with the restriction enzyme generates a 5'overhang containing the locus of interest, and a set of instructions.

177. A kit for use in the method of claim 80, comprising a set of primers used in the method, wherein the second primer contains a sequence that generates a recognition site for a restriction enzyme such that digestion with the restriction enzyme generates a 5'overhang containing the locus of interest, and a set of instructions.

178. A kit for use in the method of claim 81, comprising a set of primers used in the method, wherein the second primer contains a sequence that generates a recognition site for a restriction enzyme such that digestion with the restriction enzyme generates a 5'overhang containing the locus of interest, and a set of instructions.

179. A kit for use in the method of claim 82, comprising a set of primers used in the method, wherein the second primer contains a sequence that generates a recognition site for a restriction enzyme such that digestion with the restriction enzyme generates a 5'overhang containing the locus of interest, and a set of instructions.

180. A kit for use in the method of claim 86, comprising a set of primers used in the method, wherein the second primer contains a sequence that generates a recognition site for a restriction enzyme such that digestion with the restriction enzyme generates a 5'overhang containing the locus of interest, and a set of instructions.